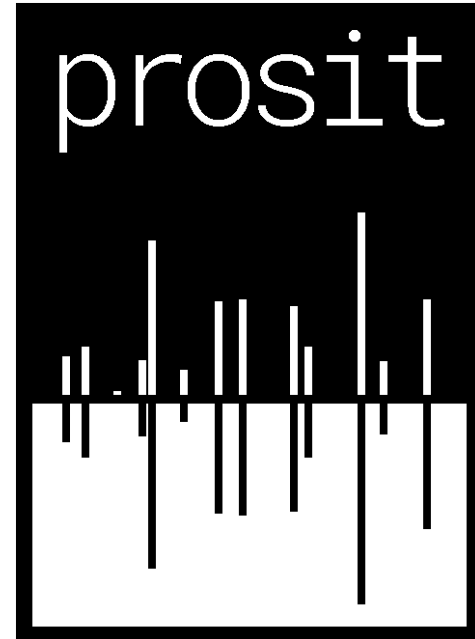


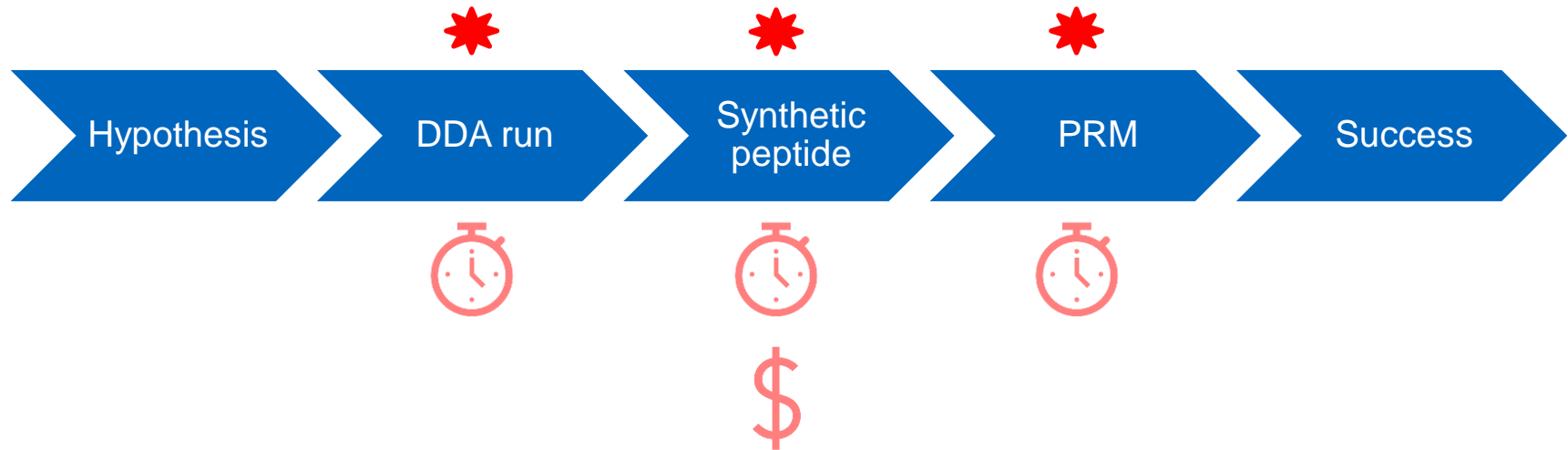
Using Prosit for PRM assay development and optimization

Tobias Schmidt

Technische Universität München

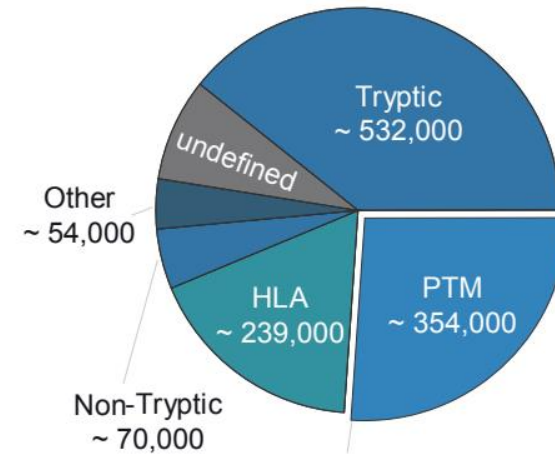
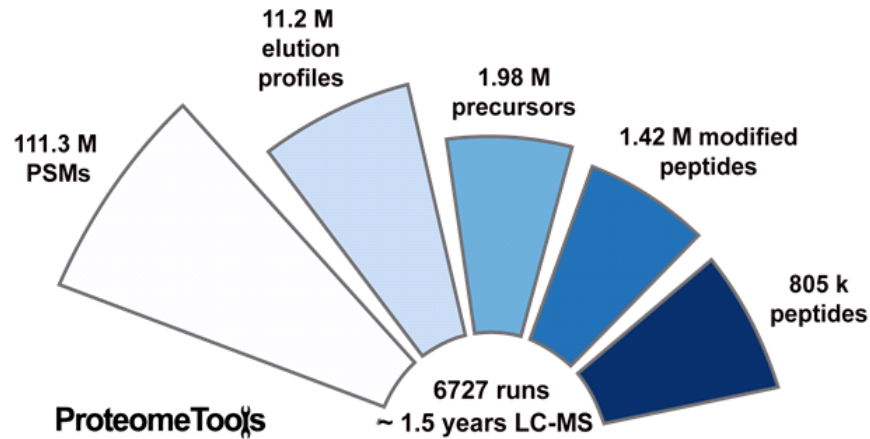


Challenges in targeted assay development

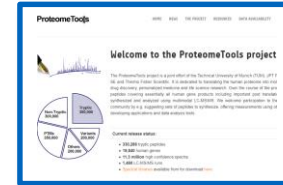
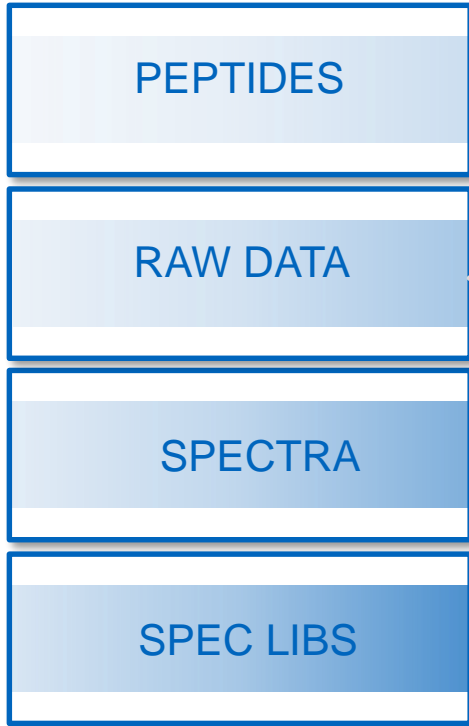


*** Can be mitigated to some extent with access to synthetic spectral libraries**

ProteomeTools: Overview

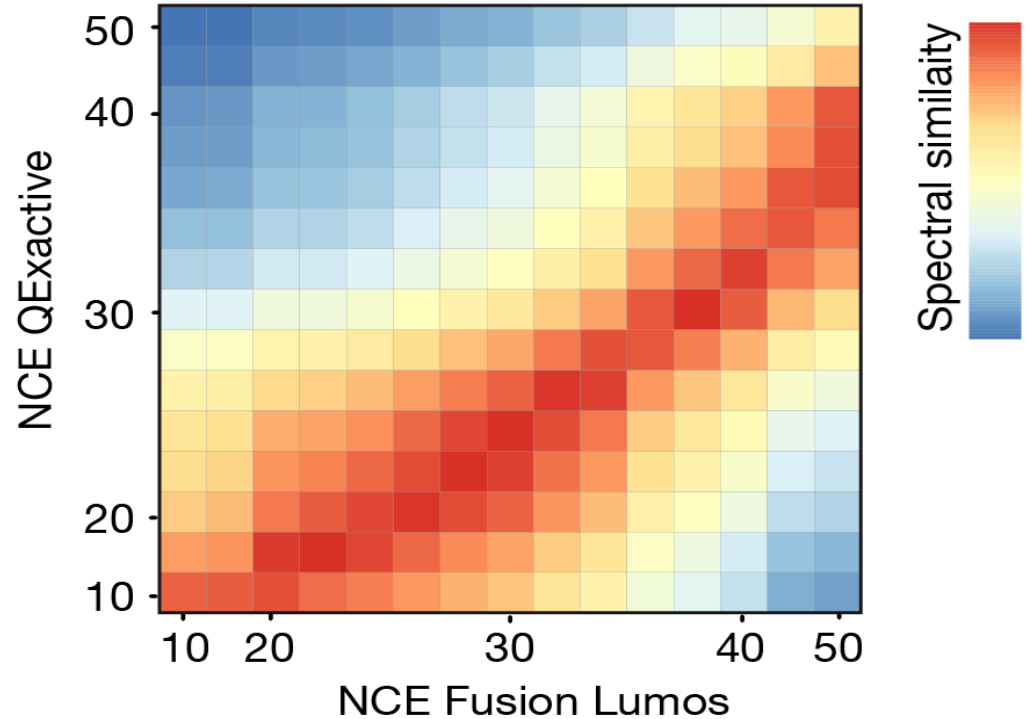
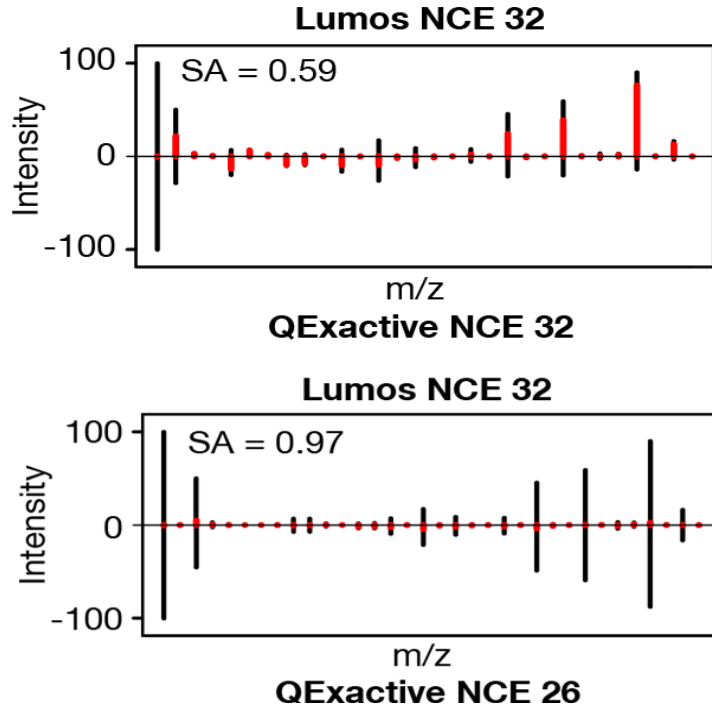


ProteomeTools: Availability








... by labeled peptides
 ... by other platforms

ProteomeTools: Transferability

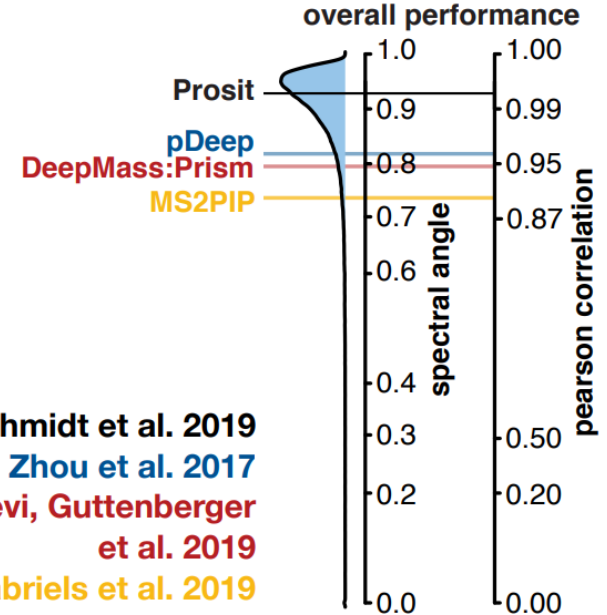
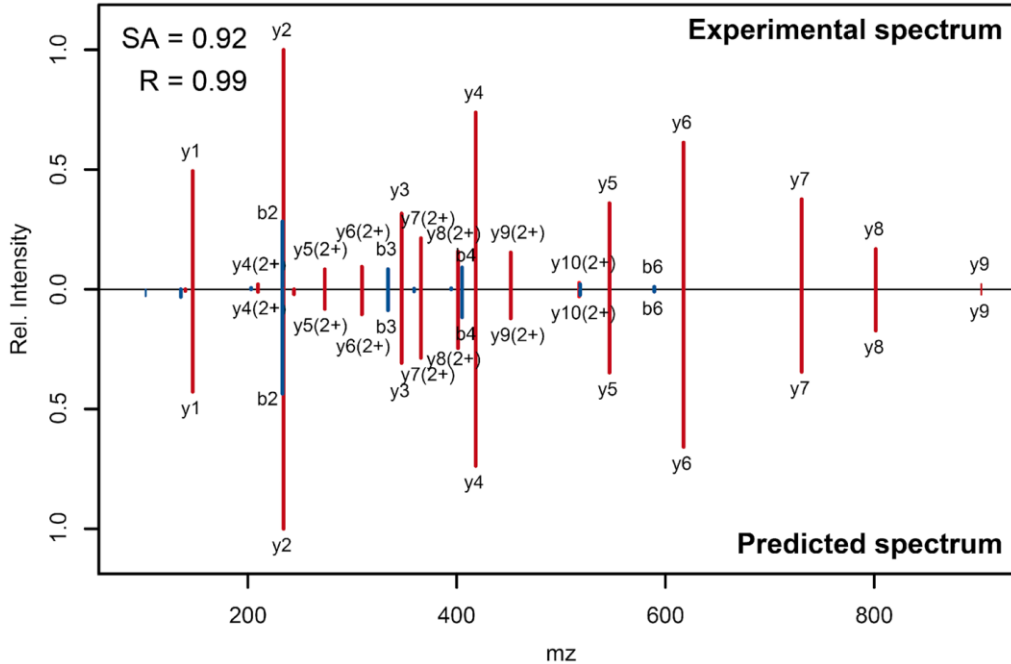


Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning

Siegfried Gessulat ^{1,2,7}, Tobias Schmidt^{1,7}, Daniel Paul Zolg¹, Patroklos Samaras ¹,
Karsten Schnatbaum³, Johannes Zerweck³, Tobias Knaute³, Julia Rechenberger¹, Bernard Delanghe⁴,
Andreas Huhmer⁵, Ulf Reimer³, Hans-Christian Ehrlich², Stephan Aiche ², Bernhard Kuster ^{1,6*}
and Mathias Wilhelm ^{1*}

Prediction of (nearly) reference-like spectra

TMTALAKAISK 3+, HCD @ NCE 30



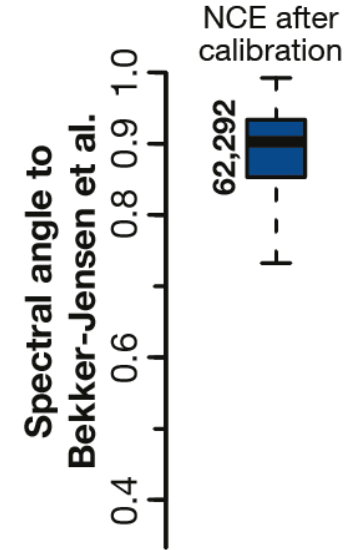
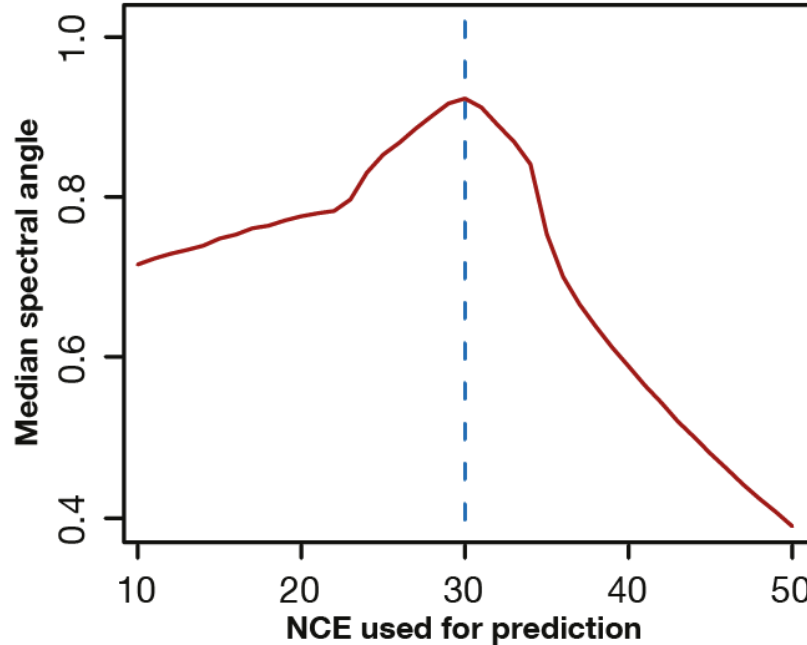
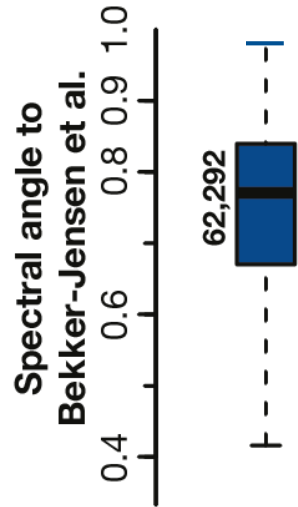
Gessulat, Schmidt et al. 2019
 Zhou et al. 2017
 Shivani, Levi, Guttenberger et al. 2019
 Gabriels et al. 2019

Collision energy calibration yields more precise predictions

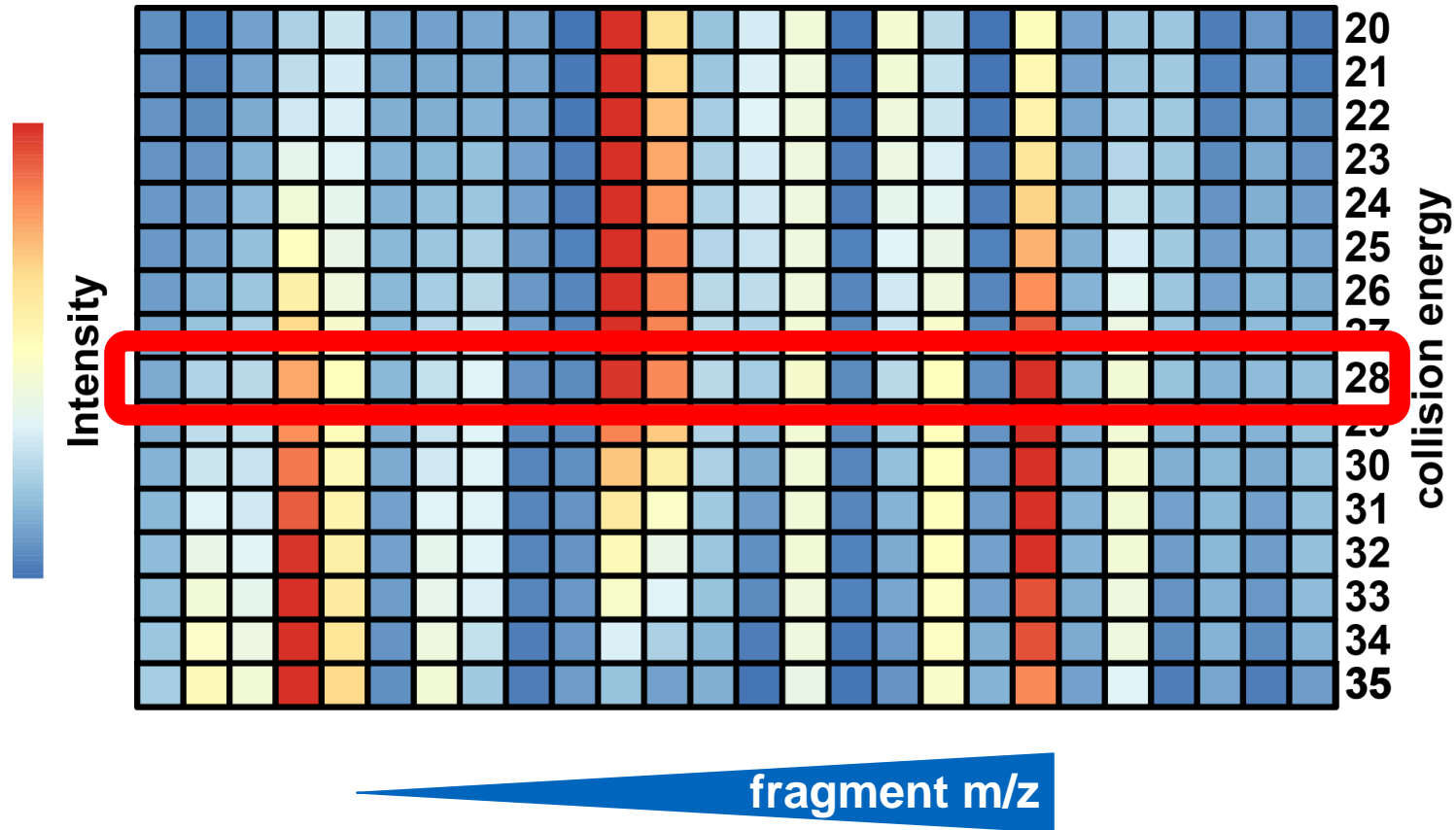
Before calibration

Calibration

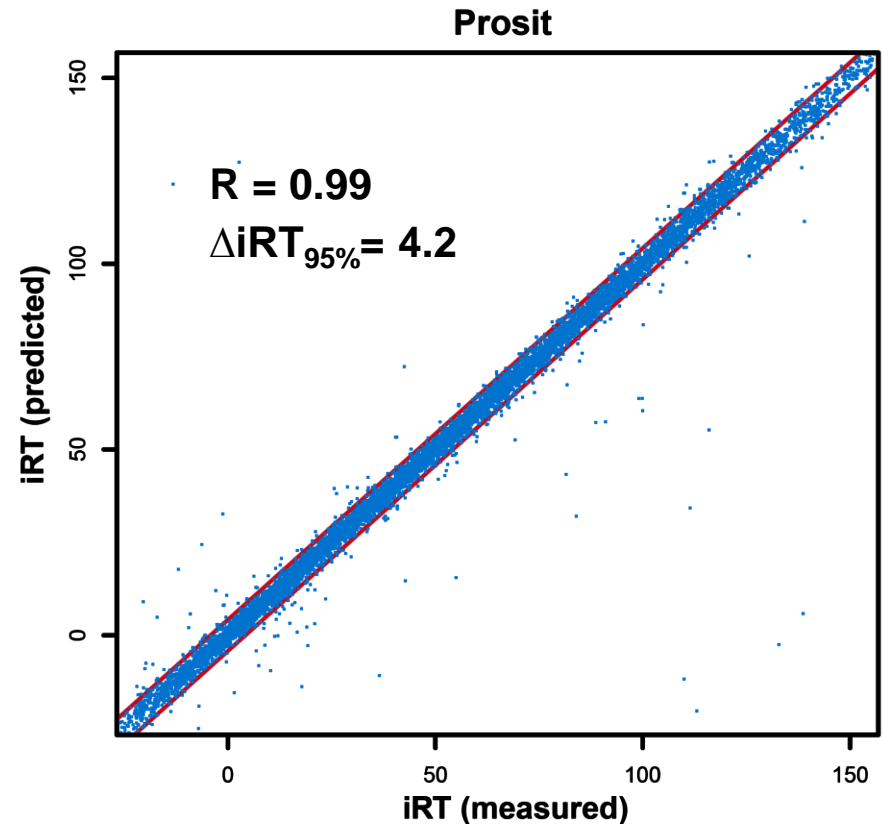
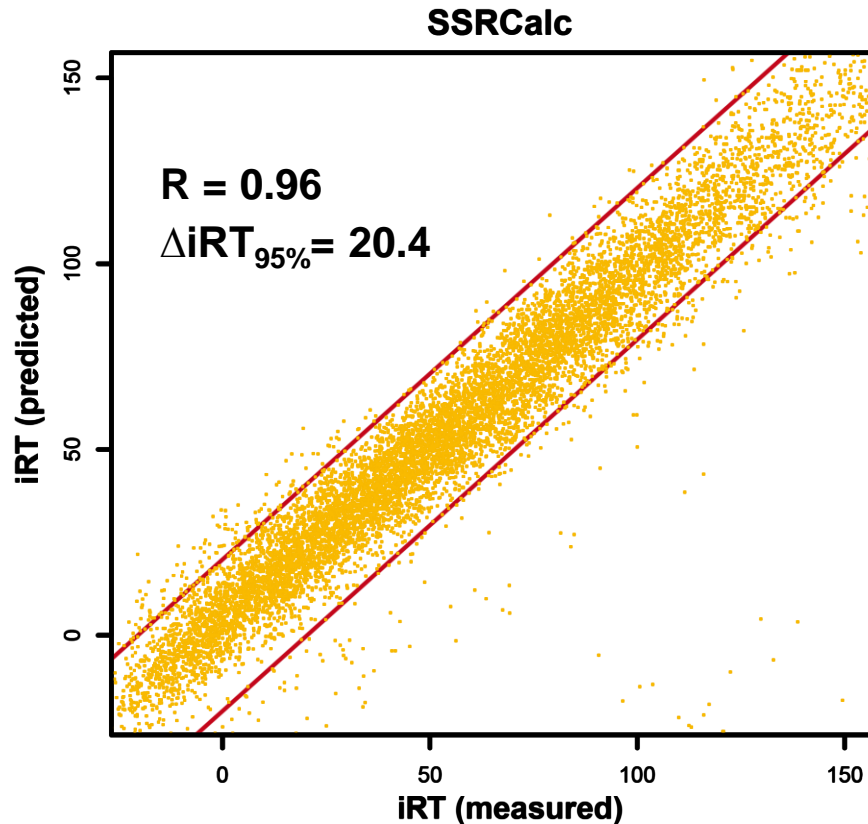
After calibration



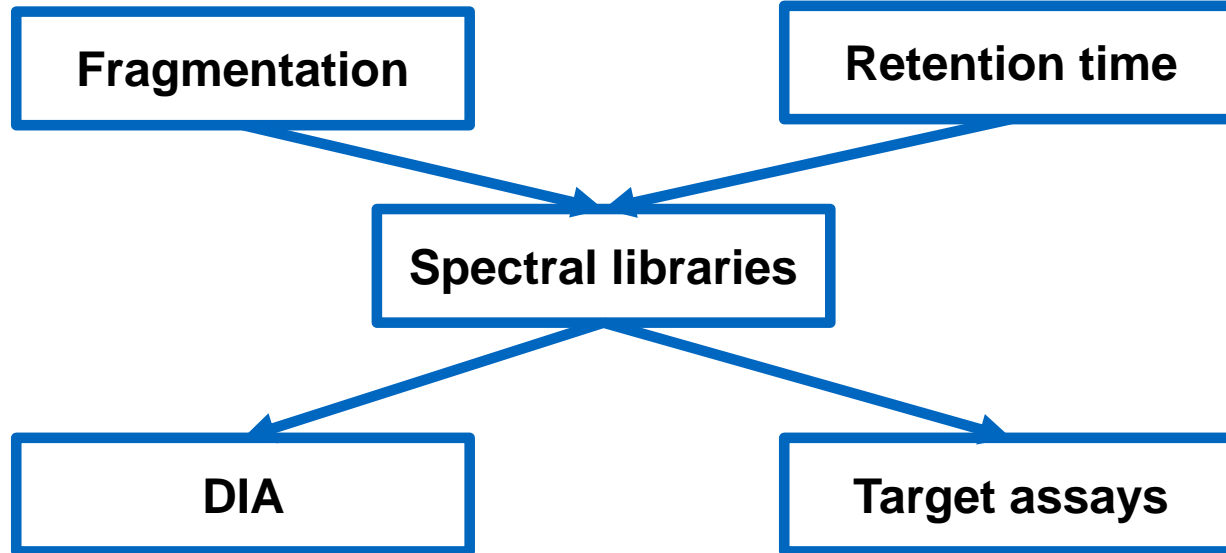
The predicted fragmentation map of GIDFKEDGNILGHK



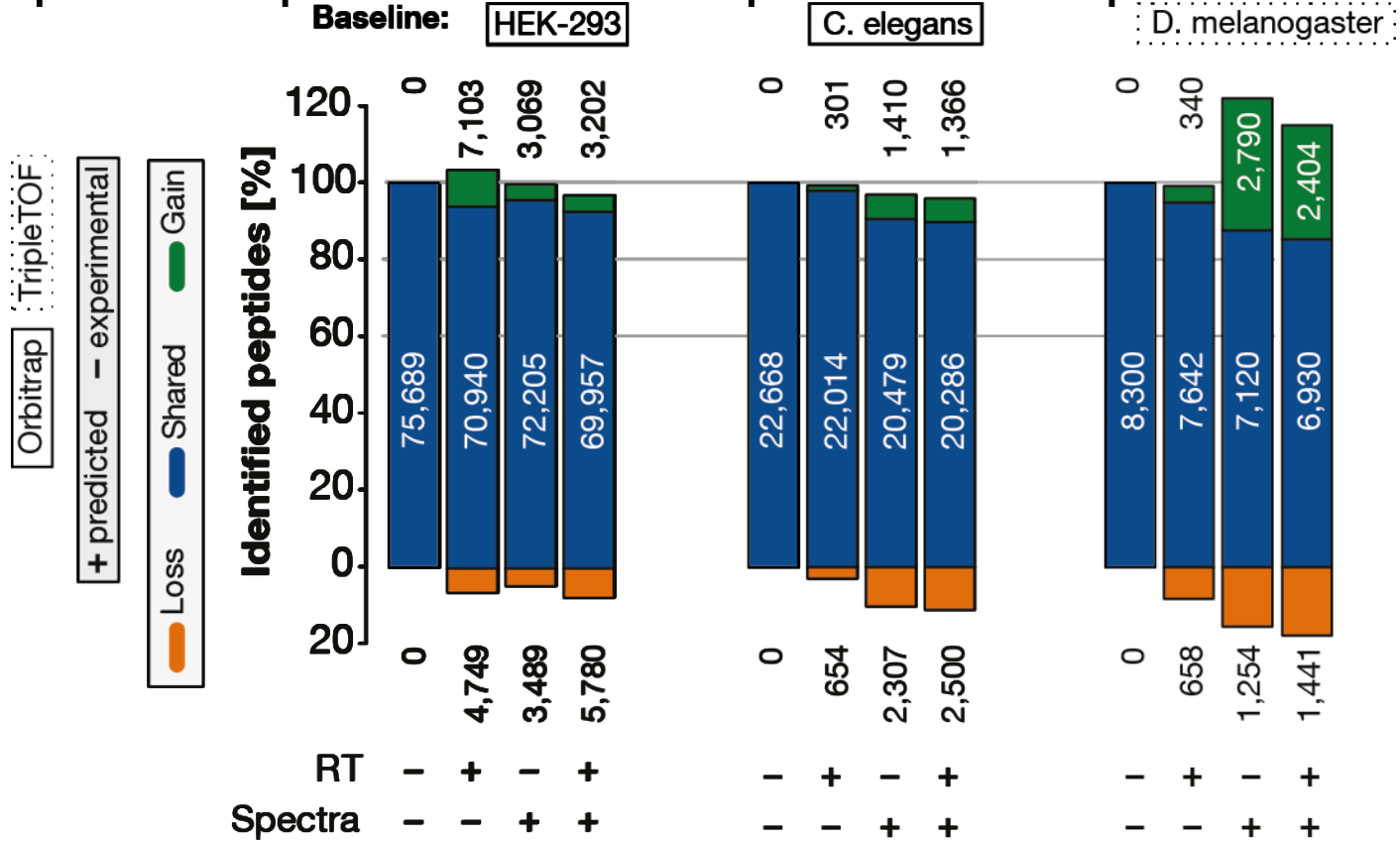
Prediction of highly accurate (indexed) retention time



Combination of predictions



Stepwise replacement of experimental spectral libraries



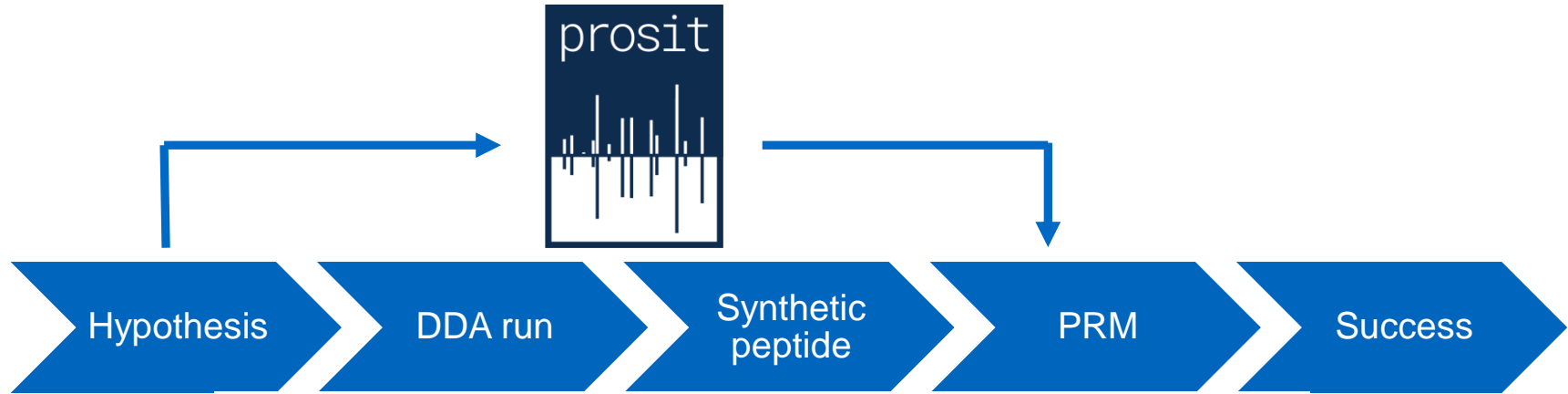
Finding a mini-Protein in *Bacillus Licheniformis*



Hypothesis: A 45 aa long hypothetical protein could be involved in malate synthesis.

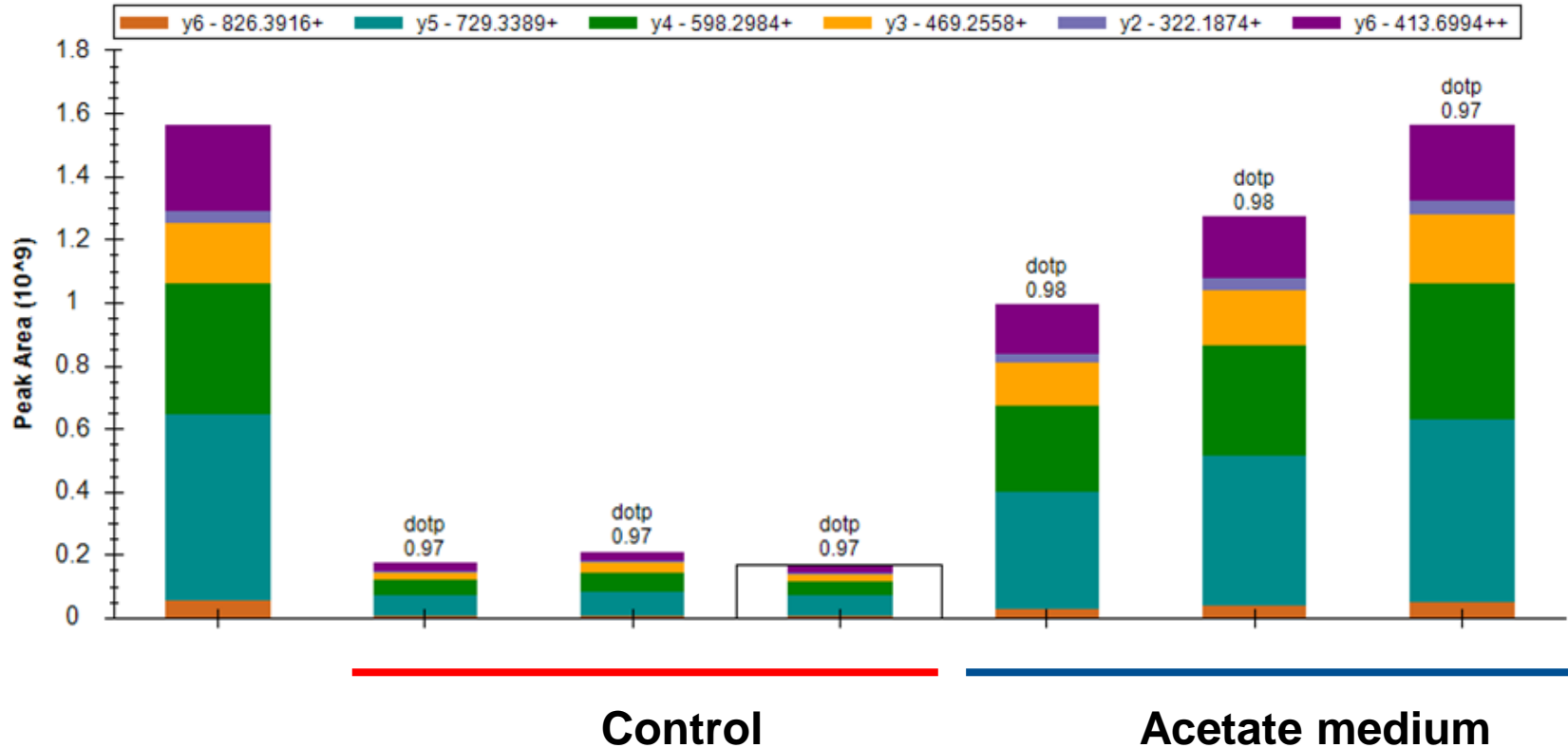
Collaboration with Professor Liebl and
Armin Ehrenreich
Chair of Microbiology (TUM)

Workflow

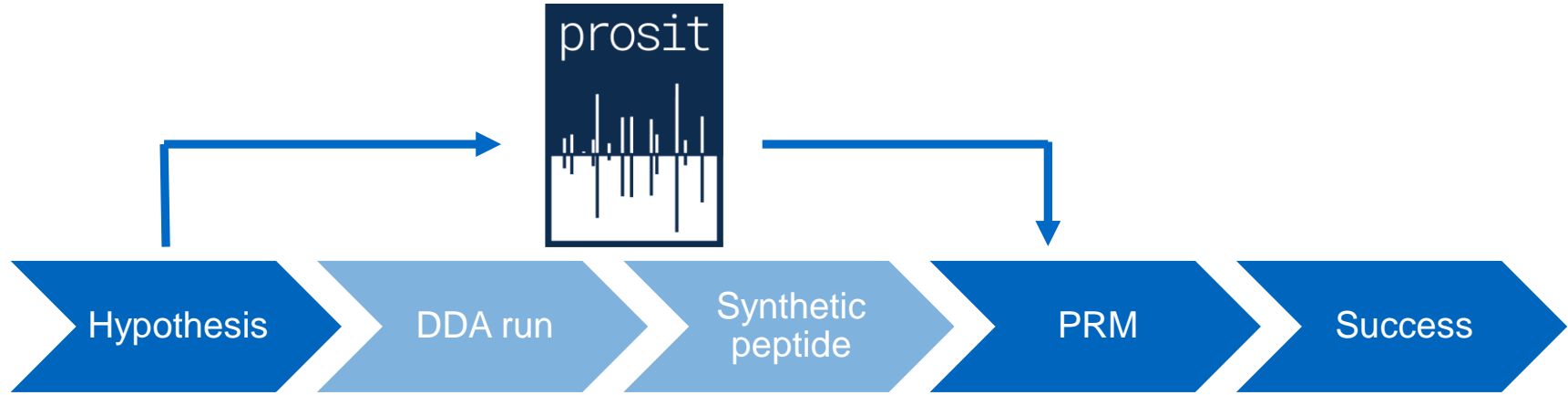


modified_sequence	collision_energy	precursor_charge
M(ox)CSDSDGLAPPQHLIR	15	2
EMPQSDPSVEPPLSQETFSDLWK	28	2
TCPVQLWVDSTPPPGTR	30	3
QSQHM(ox)TEVVR	45	5

Prosit + Skyline = ❤️



Summary



Creation and optimization of targeted assays is now possible in-silico

After ASMS we are starting a collaboration with the Skyline team to make Prosit output available in **Skyline**

Thank you for your attention



ProteomicsDB.org Team

Bernhard Kuster, Mathias Wilhelm,
Patroklos Samaras, Martin Frejno,
Siegfried Gessulat

Biognosys

Tina Ludwig
Prof Liebl
Prof. Selbach

Bavarian Center for Biomolecular Mass Spectrometry (TUM)
Chair of Microbiology (TUM)
Max-Delbrück-Centrum für Molekulare Medizin



More talks and poster about Prosit +

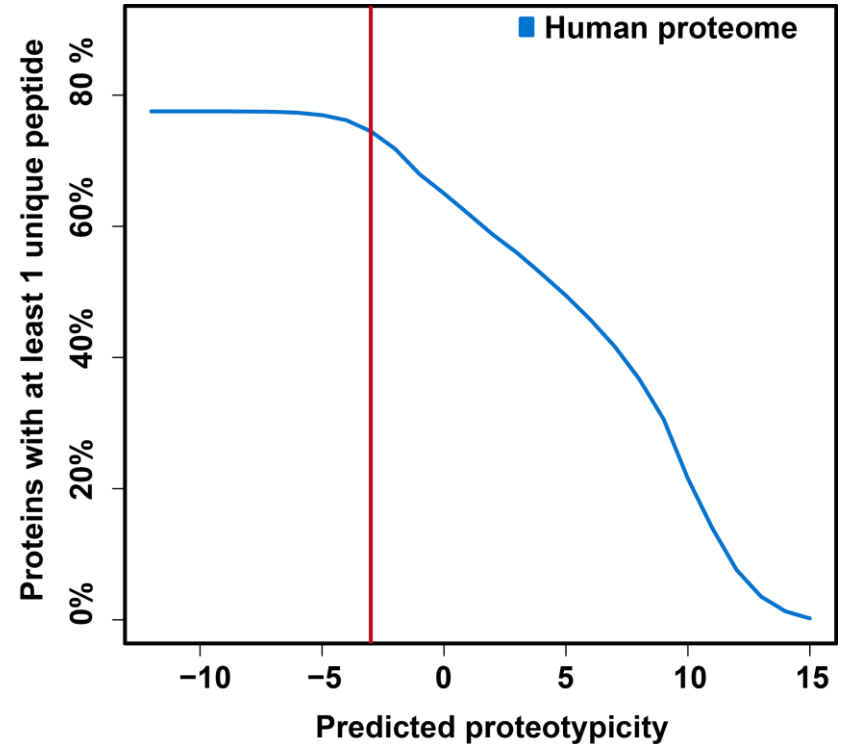
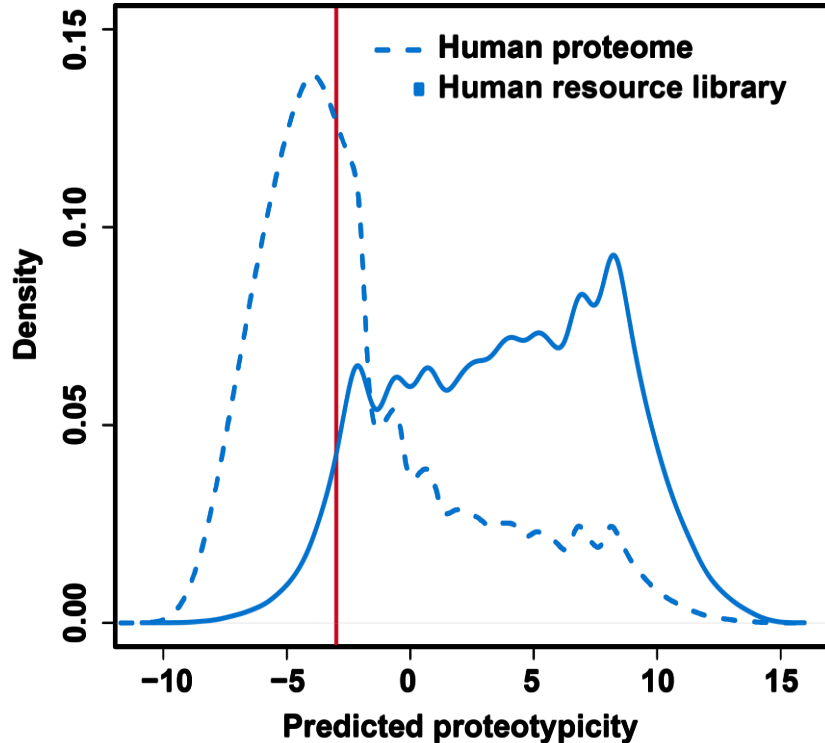
- DDA analysis (MP383)
- Proteogenomics (TP422)
- Further extensions (WP398)
- EncyclopeDIA (ThP272)

Feel free to test it on

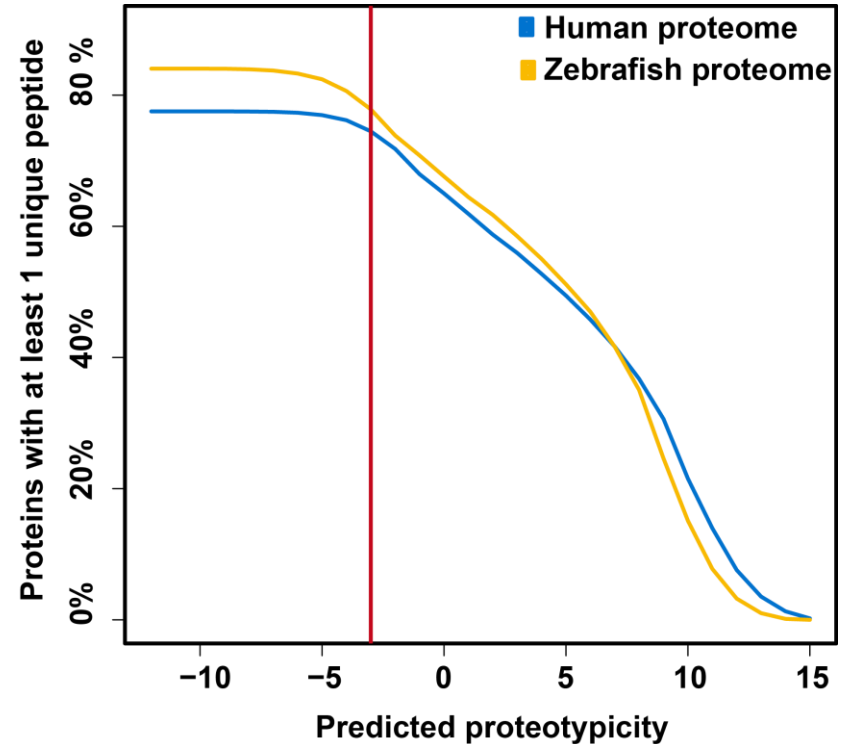
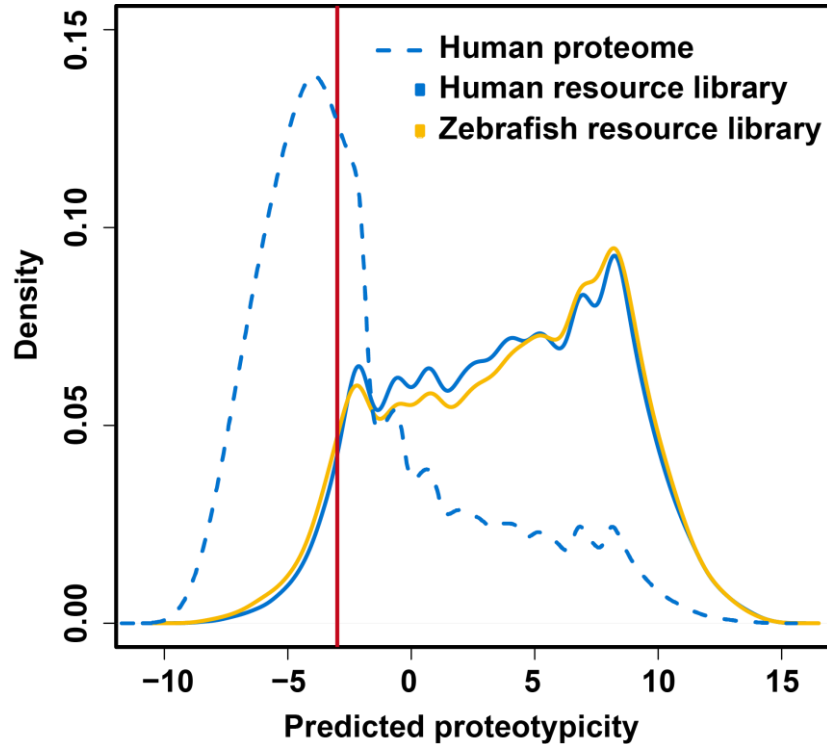
<https://proteomicsdb.org/prosit>

Data-driven reduction of spectral libraries

Prosit enables prediction of peptide proteotypicity



Proteotypicity prediction extrapolates to other organisms



Preliminary results: PTMs

